

(2)

OIEP

## RAW SEQUENCE LISTING

DATE: 07/19/2001

PATENT APPLICATION: US/09/899,513

TIME: 15:22:09

Input Set : A:\LEX-0200-USA SEQLIST.txt

Output Set: N:\CRF3\07192001\I899513.raw

PS

4 <110> APPLICANT: Hu, Yi  
 5 Turner, C. Alexander Jr.  
 6 Nepomnichy, Boris  
 7 Scoville, John  
 8 Walke, D. Wade  
 10 <120> TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding  
 the Same

12 <130> FILE REFERENCE: LEX-0200-USA  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/899,513  
 C--> 14 <141> CURRENT FILING DATE: 2000-07-05

14 <150> PRIOR APPLICATION NUMBER: US 60/217,600  
 15 <151> PRIOR FILING DATE: 2000-07-11  
 17 <160> NUMBER OF SEQ ID NOS: 8  
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 618  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: homo sapiens

ENTERED

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 29 gctcgtttca tegtgttgcc cgcggcctat gccttggcac tgggacctgg gctgccagcc 180  
 30 aacgtggcgg ccctggcaat gttcatccgc agcggcgggc gcctgggcca ggccctgctt 240  
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 32 ctcaacctact acctgggcct ggcccggagg ccgcctgcca cgcggccggg gccacctact 360  
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 34 tcgtacgcgg tcccgggcc agggcggctg cccgcctggc ccggtgccta cggbgccccg 480  
 35 cgcgcgtcgc ctgcgcttc gcctggctgg cgggcctggc ccctccctgc ctggagcacc 540  
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 37 tgctcgcggc caacgtga 618

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 40 <211> LENGTH: 205  
 41 <212> TYPE: PRT  
 42 <213> ORGANISM: homo sapiens

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 48 20 25 30  
 49 Gly Cys Ser Leu Trp Asp Asp Pro Ala Arg Phe Ile Val Val Pro Ala  
 50 35 40 45  
 51 Ala Tyr Ala Leu Ala Leu Gly Leu Gly Leu Pro Ala Asn Val Ala Ala  
 52 50 55 60  
 53 Leu Ala Met Phe Ile Arg Ser Gly Gly Arg Leu Gly Gln Ala Leu Leu  
 54 65 70 75 80  
 55 Leu Tyr Leu Phe Asn Leu Ala Leu Val Asp Glu Phe Phe Thr Leu Thr  
 56 85 90 95  
 57 Leu Gln Leu Trp Leu Thr Tyr Tyr Leu Gly Leu Ala Arg Arg Pro Pro

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59 Ala Thr Arg Pro Gly Pro Pro Thr Thr Cys Pro Pro Met Arg Arg Trp
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63 Pro Gly Pro Gly Arg Leu Pro Ala Trp Pro Gly Ala Tyr Gly Ala Pro
64 145          150          155          160
65 Arg Ala Leu Pro Ala Pro Ser Pro Gly Trp Arg Ala Trp Pro Leu Pro
66          165          170          175
67 Ala Trp Ser Thr Ala Gly Gln Ala Arg Gly Trp Pro Pro Pro Arg Trp
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69 Pro Ser Arg Pro Pro Ser Cys Trp Cys Ser Arg Pro Thr
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80 aggggcatct ctaccctctc agtcactaag gttggaaatt tccaagttat ctaggactcc      180
81 tgccctcttc tcgcttccca cagtttgtca ccaaaaactc tggagtccat accctcctct      240
82 cagcagctgc tggccagggt cggtcttcat tccctctcac atggactctg cctctagtgt      300
83 cccctccag caagggctga agaagaggag actgggggtg gagaagggtg aatgggggct      360
84 gcctttgtcg ctagcctccg cagtaacctt tcttctgcca cttcaaggtc agagatgaac      420
85 agcagtgttg gggacctggg tgttgcgggc tgcagcctct gggatgacct tgctcgcttc      480
86 atcgtggtgc ccgcggccta tgccttggca ctgggcctgg ggctgccagc caacgtggcg      540
87 gccctggcaa tggtcatccg cagcggcggg cgctggggcc aggccctgct tctctacctg      600
88 ttcaacctgg ctctggttga tgagttcttc acgctcacgc tgcagctgtg gctcacctac      660
89 tacctgggcc tggcccggag gccgcctgcc acgcggccgg ggccacctac tacgtgtcca      720
90 cctatgcggc ggtggtcttc gccgcgtca tcagcgtgtg ccgctgcggc ttcgtacggc      780
91 gtcccgggcc cagggcggtt gccgcctgg cccggtgctt acggcgcccc gcgcgcgtg      840
92 cctgcgcctt cgcttggtg gcgggcctgg cccctccctg cctggagcac cgtgggcaa      900
93 gctcggggct ggctccgcc acggtggcct tcgcggcgcc ctctctgctg gtgctcgcg      960
94 ccaacgtgag cctggcgcg gcgtcaagg cgccctctgg cccgggccc ggccctgcaa      1020
95 ccgcccgcgc gcaccggcgc gcggccaaga ccatggtcct ggggttcctg ctggtcttcg      1080
96 ccctcagtct ggcgccaac cacctgctgc tgggcacctt ggtggctggg ggggaagaca      1140
97 acggagaccg gtgtcgcgcc gcctccacgc tcgacatcct gcacaccctc agcctggcgc      1200
98 tgetgagcct caacagctgc ctggaccac tcactctgctg cttcttctg cgctcttcc      1260
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102 ctgacgcaac cacatactac cctgtagct gtgaacctcc cagtcacctt ctaggcccgc      1500
103 ggaaaatgcc ggtctcctac tcttcatggc ctttgtacct gacttgcca ggaatgatct      1560
104 ctgttcctct ctttactaa gttagttctt cttcaccctc acttctcta aagtaactcc      1620
105 ttatagggaa gcctttcttg gctggcaaca cacacacaca cacacacaca cacatacaca      1680
106 cagagtgaa tcagatcgga ktgctctttg atagctcttt tcataattgt aatcaagcaa      1740
107 ttaattgggt aatgcggtg tgggttttct tttctctctt gccagaatgt attcatgttg      1800
108 acccataaga cattatcatt ttataagcc cccaaaagtt gaattattga aattttattt      1860

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109 ccacccaatt caacttaata aattctgtgt ttaccttgw maaaaaaaaa aaaaaaaaaa 1920
110 aaatcactgc tgtatctcct gtggttgga ctgcgccttg catataataa gagctcagtg 1980
111 tatcagatgc gtgagtga aaactgaatctc attaatctta attgcttaag tactcactca 2040
112 cacattccaa gtctgtgata gcttttccct caagtgtgtg tgagattctc caagcttg 2098
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115 <211> LENGTH: 3774
116 <212> TYPE: DNA
117 <213> ORGANISM: homo sapiens
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122 gatggactgg acatcacact catgatcctg ggtatactgg catcactggt caatggagcc 180
123 tgccttccct taatgccact ggttttagga gaaatgagtg ataaccttat tagtggatgt 240
124 ctagtccaaa ctaacacatc aaattatcag aactgtactc agtctcaaga gaagctgaat 300
125 gaagatatga ctctgttgcc cctgtattat gttggaatag gtgttgctgc cttgattttt 360
126 ggttacatac agatttccct gtggattata actgcagcac gacagacca gaggattcga 420
127 aaacagtttt ttcatcagtt tttggcacag gacatcggct ggtttgatag ctgtgacatc 480
128 ggtgaactta acactcgcac gacagatgac attgacaaaa tcagtgatgg tattggagat 540
129 aagattgctc tgtttgttca aaacatgtct actttttcga ttggcctggc agttggtttg 600
130 gtttaagggt ggaaactcac cctagtgaat ctatccacgt ctcctcttat aatggcttca 660
131 ggcgcagcat gttctaggat ggtcatctca ttgccagta aggaattaag tgcctattcc 720
132 aaagctgggg ctgtggcaga agaagctctg tcatcaatcc gaacagtcac agcctttagg 780
133 gccaggaga aagaacttca aaggtataca cagaatctca aagatgcaa ggattttggc 840
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136 accatcggga ctgttcttgc tgttttcttt agtgaatcc atagcagtta ttgcattgga 1020
137 gcagcagtc ctcactttga aaccttcgca atagcccag gagctgcctt tcatattttc 1080
138 cagggtattg ataagaaacc cagtatagat aacttttcca cagctggata taaacctgaa 1140
139 tccatagaag gaactgtgga atttaaaaaat gtttctttca attatccatc aagaccatct 1200
140 atcaagattc tgaaaggctc gaatctcaga attaatctg gagagacagt cgccttggtc 1260
141 ggtctcaatg ccagtggaaa gactacggtg gtccagcttc tgcagagggt atatgatccg 1320
142 gatgatggct ttatcatggt ggatgagaat gacatcagag ctttaaatgt gcggcattat 1380
143 cgagaccata ttggagtggg tagtcaagag cctgttttgt tcgggaccac catcagtaac 1440
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151 atgtcacagg atattaaaaa agctgatgaa cagatggagt caatgacata ttctactgaa 1920
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156 ggaaataatg ataaaaccac attaaagcat gatgcagaaa tttattccat gatattcgct 2220
157 attttgggtg ttatttgctt tgtcagttat ttcatgcagg gattatttta cggcagagca 2280
158 ggggaaattt taccgatgag attaagacac ttggccttca aagccatgtt atatcaggat 2340
159 attgctggtt ttgatgaaaa ggaaaacagc acaggaggct tgacaacaat attagccata 2400

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160 gatatagcac aaattcaagg agcaacaggt tccaggattg gcgtcttaac acaaaatgca 2460
161 actaacatgg gactttcagt tatcatttcc tttatatatg gatgggagat gacattcctg 2520
162 attctgagta ttgctccagt acttgccgtg acaggaatga ttgaaaccgc agcaatgact 2580
163 ggatttgcca acaaagataa gcaagaactt aagcatgctg gaaagatagc aactgaagct 2640
164 ttggagaata tacgtactat agtgtcatta acaagggaaa aagccttcga gcaaatgtat 2700
165 gaagagatgc ttcagactca acacagaaat acctcgaaga aagcacagat tattggaagc 2760
166 tgttatgcat tcagccatgc ctttatatat tttgcctatg cagcagggtt tcgatttgga 2820
167 gcctatttaa ttcaagctgg acgaatgacc ccagagggca tgttcatagt ttttactgca 2880
168 attgcatatg gagctatggc catcggaaaa acgctcgttt tggctcctga atattccaaa 2940
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170 cgcagtcaag aagggaaaaa gccagacaca tgtgaaggga atttagagtt tcgagaagtc 3060
171 tctttcttct atccatgtcg cccagatgtt ttcacctccc gtggcttatt cctcagtatt 3120
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173 caacttctgc agagacttta tgaccccggt caaggacaag tgctgtttga tgggtgtggat 3240
174 gcaaaagaat tgaatgtaca gtggctccgt tcccaaatag caatcgttcc tcaagagcct 3300
175 gtgctcttca actgcagcat tgctgagaac atcgccatg gtgacaacag ccgtgtgggtg 3360
176 ccattagatg agatcaaaga agccgcaa atgcgcaaata tccattcttt tattgaaggt 3420
177 ctccctgaga aatacaaac acaagttgga ctgaaaggag cacagcttcc tggcggccag 3480
178 aaacaaagac tagctattgc aagggtctct ctccaaaaac ccaaaatttt attgktggat 3540
179 gaggccactt cagccctcga taatgacagt gagaagggtg ttcagcatgc ccttgataaa 3600
180 gccaggacgg gaaggacatg cctagtggtc actcacaggc tctctgcaat tcagaacgca 3660
181 gatttgatag tggttctgca caatggaaag ataaaggaac aaggaactca tcaagagctc 3720
182 ctgagaaatc gagacatata ttttaagtta gtgaatgcac agtcagtgca gtga 3774
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 1257
186 <212> TYPE: PRT
187 <213> ORGANISM: homo sapiens
189 <220> FEATURE:
190 <221> NAME/KEY: VARIANT
191 <222> LOCATION: (1)...(1257)
192 <223> OTHER INFORMATION: Xaa = Any Amino Acid
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198 20 25 30
199 Ser Ile Glu Ile Phe Arg Phe Ala Asp Gly Leu Asp Ile Thr Leu Met
200 35 40 45
201 Ile Leu Gly Ile Leu Ala Ser Leu Val Asn Gly Ala Cys Leu Pro Leu
202 50 55 60
203 Met Pro Leu Val Leu Gly Glu Met Ser Asp Asn Leu Ile Ser Gly Cys
204 65 70 75 80
205 Leu Val Gln Thr Asn Thr Ser Asn Tyr Gln Asn Cys Thr Gln Ser Gln
206 85 90 95
207 Glu Lys Leu Asn Glu Asp Met Thr Leu Leu Pro Leu Tyr Tyr Val Gly
208 100 105 110
209 Ile Gly Val Ala Ala Leu Ile Phe Gly Tyr Ile Gln Ile Ser Leu Trp
210 115 120 125
211 Ile Ile Thr Ala Ala Arg Gln Thr Lys Arg Ile Arg Lys Gln Phe Phe

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216      165      170      175
217 Gly Ile Gly Asp Lys Ile Ala Leu Leu Phe Gln Asn Met Ser Thr Phe
218      180      185      190
219 Ser Ile Gly Leu Ala Val Gly Leu Val Lys Gly Trp Lys Leu Thr Leu
220      195      200      205
221 Val Thr Leu Ser Thr Ser Pro Leu Ile Met Ala Ser Ala Ala Ala Cys
222      210      215      220
223 Ser Arg Met Val Ile Ser Leu Pro Ser Lys Glu Leu Ser Ala Tyr Ser
224 225      230      235      240
225 Lys Ala Gly Ala Val Ala Glu Glu Val Leu Ser Ser Ile Arg Thr Val
226      245      250      255
227 Ile Ala Phe Arg Ala Gln Glu Lys Glu Leu Gln Arg Tyr Thr Gln Asn
228      260      265      270
229 Leu Lys Asp Ala Lys Asp Phe Gly Ile Lys Arg Thr Ile Ala Ser Lys
230      275      280      285
231 Val Ser Leu Gly Ala Val Tyr Phe Phe Met Asn Gly Thr Tyr Gly Leu
232      290      295      300
233 Ala Phe Trp Tyr Gly Thr Ser Leu Ile Leu Asn Gly Glu Pro Gly Tyr
234 305      310      315      320
235 Thr Ile Gly Thr Val Leu Ala Val Phe Phe Ser Val Ile His Ser Ser
236      325      330      335
237 Tyr Cys Ile Gly Ala Ala Val Pro His Phe Glu Thr Phe Ala Ile Ala
238      340      345      350
239 Arg Gly Ala Ala Phe His Ile Phe Gln Val Ile Asp Lys Lys Pro Ser
240      355      360      365
241 Ile Asp Asn Phe Ser Thr Ala Gly Tyr Lys Pro Glu Ser Ile Glu Gly
242      370      375      380
243 Thr Val Glu Phe Lys Asn Val Ser Phe Asn Tyr Pro Ser Arg Pro Ser
244 385      390      395      400
245 Ile Lys Ile Leu Lys Gly Leu Asn Leu Arg Ile Lys Ser Gly Glu Thr
246      405      410      415
247 Val Ala Leu Val Gly Leu Asn Ala Ser Gly Lys Ser Thr Val Val Gln
248      420      425      430
249 Leu Leu Gln Arg Leu Tyr Asp Pro Asp Asp Gly Phe Ile Met Val Asp
250      435      440      445
251 Glu Asn Asp Ile Arg Ala Leu Asn Val Arg His Tyr Arg Asp His Ile
252      450      455      460
253 Gly Val Val Ser Gln Glu Pro Val Leu Phe Gly Thr Thr Ile Ser Asn
254 465      470      475      480
W--> 255 Asn Ile Lys Tyr Gly Xaa Asp Asp Val Thr Asp Glu Glu Met Glu Arg
256      485      490      495
257 Ala Ala Arg Glu Ala Asn Ala Tyr Asp Phe Ile Met Glu Phe Pro Asn
258      500      505      510
259 Lys Phe Asn Thr Leu Val Gly Glu Lys Gly Ala Gln Met Ser Gly Gly
260      515      520      525

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Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7